What is claimed is:

1. A computer system comprising:

a database correlating the presence of at least one mutation in an HIV reverse transcriptase and resistance of at least one strain of HIV to a reverse transcriptase inhibitor, comprising

a first set of records corresponding to a correlation between at least one first mutation chosen from 88E, 101H, 101N, 101P, 101Q, 101T, 103H, 103S, 179I, 179E, 181V, 190E, 190S, 190T or the combination of 103R and 179D, and resistance to at least one non-nucleoside reverse transcriptase inhibitor; and

a second set of records corresponding to a correlation between at least one second mutation chosen from 69S-[S-S], 184G, 184L, 215 V, 44D, 44A, or 118I, and resistance to at least one nucleoside reverse transcriptase inhibitor.

2. The computer system according to claim 1, wherein said at least one first mutation is 103S and said HIV reverse transcriptase further comprises at least one additional mutation 101P.

3. The computer system according to claim 1, wherein said at least one second mutation is chosen from 44D, 44A or 118I and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 41L, 67N, 69D, 70R, 210W, 211K, 214F, 215Y, 215F, 219Q or 219E.

4. The computer system according to claim 3 wherein said at least one second mutation is a combination of mutations chosen from 118I and 44D; 118I and 44A; and 118I, 44A and 44D.

5. The computer system according to claim 1 wherein said at least one second mutation is 69S-[S-S] and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 62V, 210W, 215Y.

6. A computer system comprising:

a database correlating the presence of at least one mutation in a HIV protease and resistance of at least one strain of HIV to a protease inhibitor, comprising

a first set of records corresponding to a correlation between at least one first mutation chosen from 88T and the combination of mutations 33F and 90M.

7. A method of evaluating the effectiveness of an antiviral therapy of an HIV-infected patient comprising:

(i) collecting a sample from an HIV-infected patient;

(ii) determining whether the sample comprises at least one nucleic acid chosen from:

SUB A3 (a) a first nucleic acid encoding HIV reverse transcriptase having at least one mutation chosen from 88E, 101H, 101N, 101P, 101Q, 101T, 103H, 103S, 179I, 179E, 181V, 190E, 190S, 190T and the combination of mutations 103 R and 179D,

in which the presence of said at least one mutation correlates with resistance to at least one NNRTI;

(b) a second nucleic acid encoding HIV reverse transcriptase having at least one mutation chosen from 69S-[S-S], 184G, 184L, 215 V, 44D, 44A, and 118I,

in which the presence of said at least one mutation correlates with resistance to at least one NRTI; and

(c) a third nucleic acid encoding HIV protease having at least one mutation chosen from 88T and the combination of mutations 33F and 90M,

in which the presence of said at least one mutation correlates with resistance to at least one PI; and

(iii) using the presence of said at least one nucleic acid to evaluate the effectiveness of said antiviral therapy.

8. The method according to claim 7 wherein said at least one mutation of said first nucleic acid is 103S and said HIV reverse transcriptase further comprises at least one additional mutation 101P.

9. The method according to claim 7 wherein said at least one mutation of said second nucleic acid is chosen from 44D, 44A and 118I and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 41L, 67N, 69D, 70R, 210W, 211K, 214F, 215Y, 215F, 219Q and 219E.

10. The method according to claim 9 wherein said at least one mutation of said second nucleic acid is a combination of mutations chosen from 118I and 44D; 118I and 44A; and 118I, 44A and 44D.

11. The method according to claim 7 wherein said at least one mutation of said second nucleic acid is 69S-[S-S] and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 62V, 210W, 215Y.

12. A method of identifying a drug effective against NNRTI resistant strains of HIV, comprising:

(a) providing at least one strain of HIV comprising HIV reverse transcriptase containing at least one mutation chosen from 88E, 101H, 101N, 101P, 101Q, 101T, 103H, 103S, 179I, 179E, 181V, 190E, 190S, 190T or the combination of mutations 103 R and 179D;

(b) determining a phenotypic response of said drug to said strain of HIV; and

(c) using said phenotypic response to determine the effectiveness of said drug.

13. A drug identified using the method of claim 12.

14. The method of claim 12 wherein said phenotypic response is determined using the recombinant virus assay.

15. The method according to claim 12 wherein said at least one mutation is 103S and said HIV reverse transcriptase further comprises at least one additional mutation 101P.

16. A method of identifying a drug effective against NRTI resistant strains of HIV, comprising:

(a) providing at least one strain of HIV comprising HIV reverse transcriptase containing at least one mutation chosen from 69S-[S-S], 184G, 184L, 215 V, 44D, 44A, or 118I;

(b) determining a phenotypic response of said drug to said strain of HIV; and

(c) using said phenotypic response to determine the effectiveness of said drug.

17. A drug identified using the method of claim 16.

18. The method of claim 16 wherein said phenotypic response is determined using the recombinant virus assay.

19. The method according to claim 16 wherein said at least one mutation is chosen from 44D, 44A and 118I and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 41L, 67N, 69D, 70R, 210W, 211K, 214F, 215Y, 215F, 219Q or 219E.

20. The method according to claim 19 wherein said at least one mutation is a combination of mutations chosen from 118I and 44D; 118I and 44A; or 118I, 44A and 44D.

21. The method according to claim 16 wherein said at least one mutation is 69S-[S-S] and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 62V, 210W, or 215Y.

22. A method of identifying a drug effective against PI resistant strains of HIV, the comprising:

(a) providing at least one strain of HIV comprising HIV protease containing at least one mutation chosen from 88T or the combination of mutations 33F and 90M;

(b) determining a phenotypic response of said drug to said strain of HIV; and

(c) using said phenotypic response to determine the effectiveness of said drug.

23. A drug identified using the method of claim 22.

24. The method of claim 22 wherein said phenotypic response is determined using the recombinant virus assay.

25. A method of designing a therapy for treating a patient infected with HIV comprising

(i) collecting a sample from an HIV-infected patient;

(ii) determining whether the sample comprises at least one nucleic acid chosen from:

(a) a first nucleic acid encoding HIV reverse transcriptase having at least one mutation chosen from 88E, 101H, 101N, 101P, 101Q, 101T, 103H, 103S, 179I, 179E, 181V, 190E, 190S, 190T and the combination of mutations 103 R and 179D,

in which the presence of said at least one mutation correlates with resistance to at least one NNRTI;

(b) a second nucleic acid encoding HIV reverse transcriptase having at least one mutation chosen from 69S-[S-S], 184G, 184L, 215 V, 44D, 44A, and 118I,

in which the presence of said at least one mutation correlates with resistance to at least one NRTI; and

(c) a third nucleic acid encoding HIV protease having at least one mutation chosen from 88T and the combination of mutations 33F and 90M,

in which the presence of said at least one mutation correlates with resistance to at least one PI; and

(iii) using the presence of said at least one nucleic acid to design the therapy for said patient.

26. The method according to claim 25 wherein said at least one mutation of said first nucleic acid is 103S and said HIV reverse transcriptase further comprises at least one additional mutation 101P.

27. The method according to claim 25 wherein said at least one mutation of said second nucleic acid is chosen from 44D, 44A and 118I and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 41L, 67N, 69D, 70R, 210W, 211K, 214F, 215Y, 215F, 219Q and 219E.

28. The method according to claim 27 wherein said at least one mutation of said second nucleic acid is chosen from a combination of mutations chosen from 118I and 44D; 118I and 44A; and 118I, 44A and 44D.

29. The method according to claim 25 wherein said at least one mutation of said second nucleic acid is 69S-[S-S] and said HIV reverse transcriptase further comprises at least one additional mutation chosen from 62V, 210W, 215Y.

30. A method for determining drug sensitivity of an HIV population circulating in a patient comprising

(a) collecting a sample from the patient;

(b) determining a genetic sequence of HIV genetic material from the sample;

(c) determining whether at least one mutation is present in the genetic sequence;

(d) identifying if the mutation matches a known drug resistance-associated mutation; and

(e) generating a report that lists antiviral drugs for which known drug resistance-associated mutations have been identified, wherein the report is used to determine drug sensitivity of the HIV population circulating in the patient.